



1

SEQUENCE LISTING

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NO, DAVID
SAEZ, ENRIQUE

<120> METHODS FOR MODULATING EXPRESSION OF EXOGENOUS GENES IN
MAMMALIAN SYSTEMS, AND PRODUCTS REALTED THERETO

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<140> 09/042,488

<141> 1998-03-16

<150> 08/974,530

<151> 1997-11-19

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<151> 1996-04-05

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Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
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Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro	
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Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys	
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Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg	
85 90 95	
gat gat ctc tcg cct tcg agc agc ttg aac gga tac tcg gcg aac gaa	336
Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu	
100 105 110	
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Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln	
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Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr	
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Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile	
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Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys	
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cgc caa atg ttc tcg atg aag gtg gac aac gtc gaa tac gcg ctt ctc	1296
Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu	
420 425 430	

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Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala	
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Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn	
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Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser	
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atg ggt gta gcc ctg cat tcg cac caa gag cag ctt atc ggg gga gtg 2208
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His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
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Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg
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Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln
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Pro	Ala	Thr	Thr	Ser	Ser	Ile	Thr	Ala	Ala	Val	Thr	Ala	Ser	Ser	Thr	675	680	685	
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VpEcR

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Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
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Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
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His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
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Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg
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Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val
145 150 155 160

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ctc	acg	gtc	cag	ttg	att	gtt	gag	ttt	gct	aaa	ggg	cta	cca	gcg	ttt	1056
Leu	Thr	Val	Gln	Leu	Ile	Val	Glu	Phe	Ala	Lys	Gly	Leu	Pro	Ala	Phe	
			340					345					350			
aca	aag	ata	ccc	cag	gag	gac	cag	atc	acg	tta	cta	aag	gcc	tgc	tcg	1104
Thr	Lys	Ile	Pro	Gln	Glu	Asp	Gln	Ile	Thr	Leu	Leu	Lys	Ala	Cys	Ser	
		355					360					365				
tcg	gag	gtg	atg	atg	ctg	cgt	atg	gca	cga	cgc	tat	gac	cac	agc	tcg	1152
Ser	Glu	Val	Met	Met	Leu	Arg	Met	Ala	Arg	Arg	Tyr	Asp	His	Ser	Ser	
	370					375					380					

gac tca ata ttc ttc gcg aat aat aga tca tat acg cgg gat tct tac	1200
Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr	
385 390 395 400	
aaa atg gcc gga atg gct gat aac att gaa gac ctg ctg cat ttc tgc	1248
Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys	
405 410 415	
cgc caa atg ttc tcg atg aag gtg gac aac gtc gaa tac gcg ctt ctc	1296
Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu	
420 425 430	
act gcc att gtg atc ttc tcg gac cgg ccg ggc ctg gag aag gcc caa	1344
Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln	
435 440 445	
cta gtc gaa gcg atc cag agc tac tac atc gac acg cta cgc att tat	1392
Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr	
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ata ctc aac cgc cac tgc ggc gac tca atg agc ctc gtc ttc tac gca	1440
Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala	
465 470 475 480	
aag ctg ctc tcg atc ctc acc gag ctg cgt acg ctg ggc aac cag aac	1488
Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn	
485 490 495	
gcc gag atg tgt ttc tca cta aag ctc aaa aac cgc aaa ctg ccc aag	1536
Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys	
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ttc ctc gag gag atc tgg gac gtt cat gcc atc ccg cca tcg gtc cag	1584
Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln	
515 520 525	
tcg cac ctt cag att acc cag gag gag aac gag cgt ctc gag cgg gct	1632
Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala	
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gag cgt atg cgg gca tcg gtt ggg ggc gcc att acc gcc ggc att gat	1680
Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp	
545 550 555 560	
tgc gac tct gcc tcc act tcg gcg gcg gca gcc gcg gcc cag cat cag	1728
Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Ala Gln His Gln	
565 570 575	
cct cag cct cag ccc cag ccc caa ccc tcc tcc ctg acc cag aac gat	1776
Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp	
580 585 590	
tcc cag cac cag aca cag ccg cag cta caa cct cag cta cca cct cag	1824
Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln	
595 600 605	

ctg	caa	ggt	caa	ctg	caa	ccc	cag	ctc	caa	cca	cag	ctt	cag	acg	caa	1872
Leu	Gln	Gly	Gln	Leu	Gln	Pro	Gln	Leu	Gln	Pro	Gln	Leu	Gln	Thr	Gln	
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Leu	Gln	Pro	Gln	Ile	Gln	Pro	Gln	Pro	Gln	Leu	Leu	Pro	Val	Ser	Ala	
	625				630					635					640	
ccc	gtg	ccc	gcc	tcc	gta	acc	gca	cct	ggt	tcc	ttg	tcc	gcg	gtc	agt	1968
Pro	Val	Pro	Ala	Ser	Val	Thr	Ala	Pro	Gly	Ser	Leu	Ser	Ala	Val	Ser	
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acg	agc	agc	gaa	tac	atg	ggc	gga	agt	gcg	gcc	ata	gga	ccc	atc	acg	2016
Thr	Ser	Ser	Glu	Tyr	Met	Gly	Gly	Ser	Ala	Ala	Ile	Gly	Pro	Ile	Thr	
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ccg	gca	acc	acc	agc	agt	atc	acg	gct	gcc	gtt	acc	gct	agc	tcc	acc	2064
Pro	Ala	Thr	Thr	Ser	Ser	Ile	Thr	Ala	Ala	Val	Thr	Ala	Ser	Ser	Thr	
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aca	tca	gcg	gta	ccg	atg	ggc	aac	gga	gtt	gga	gtc	ggt	gtt	ggg	gtg	2112
Thr	Ser	Ala	Val	Pro	Met	Gly	Asn	Gly	Val	Gly	Val	Gly	Val	Gly	Val	
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ggc	ggc	aac	gtc	agc	atg	tat	gcg	aac	gcc	cag	acg	gcg	atg	gcc	ttg	2160
Gly	Gly	Asn	Val	Ser	Met	Tyr	Ala	Asn	Ala	Gln	Thr	Ala	Met	Ala	Leu	
	705				710				715					720		
atg	ggt	gta	gcc	ctg	cat	tcg	cac	caa	gag	cag	ctt	atc	ggg	gga	gtg	2208
Met	Gly	Val	Ala	Leu	His	Ser	His	Gln	Glu	Gln	Leu	Ile	Gly	Gly	Val	
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gcg	gtt	aag	tcg	gag	cac	tcg	acg	act	gca	tag						2241
Ala	Val	Lys	Ser	Glu	His	Ser	Thr	Thr	Ala							
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<211> 746

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant
VpEcR

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Gly	Glu	Asp	Val	Ala	Met	Ala	His	Ala	Asp	Ala	Leu	Asp	Asp	Phe	Asp	
			20					25						30		
Leu	Asp	Met	Leu	Gly	Asp	Gly	Asp	Ser	Pro	Gly	Pro	Gly	Phe	Thr	Pro	
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His	Asp	Ser	Ala	Pro	Tyr	Gly	Ala	Leu	Asp	Met	Ala	Asp	Phe	Glu	Phe	
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Glu	Gln	Met	Phe	Thr	Asp	Ala	Leu	Gly	Ile	Asp	Glu	Tyr	Gly	Gly	Lys	65	70	75	80
Leu	Leu	Gly	Thr	Ser	Arg	Arg	Ile	Ser	Asn	Ser	Ile	Ser	Ser	Gly	Arg	85	90	95	
Asp	Asp	Leu	Ser	Pro	Ser	Ser	Ser	Leu	Asn	Gly	Tyr	Ser	Ala	Asn	Glu	100	105	110	
Ser	Cys	Asp	Ala	Lys	Lys	Ser	Lys	Lys	Gly	Pro	Ala	Pro	Arg	Val	Gln	115	120	125	
Glu	Glu	Leu	Cys	Leu	Val	Cys	Gly	Asp	Arg	Ala	Ser	Gly	Tyr	His	Tyr	130	135	140	
Asn	Ala	Leu	Thr	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Arg	Arg	Ser	Val	145	150	155	160
Thr	Lys	Ser	Ala	Val	Tyr	Cys	Cys	Lys	Phe	Gly	Arg	Ala	Cys	Glu	Met	165	170	175	
Asp	Met	Tyr	Met	Arg	Arg	Lys	Cys	Gln	Glu	Cys	Arg	Leu	Lys	Lys	Cys	180	185	190	
Leu	Ala	Val	Gly	Met	Arg	Pro	Glu	Cys	Val	Val	Pro	Glu	Asn	Gln	Cys	195	200	205	
Ala	Met	Lys	Arg	Arg	Glu	Lys	Lys	Ala	Gln	Lys	Glu	Lys	Asp	Lys	Met	210	215	220	
Thr	Thr	Ser	Pro	Ser	Ser	Gln	His	Gly	Gly	Asn	Gly	Ser	Leu	Ala	Ser	225	230	235	240
Gly	Gly	Gly	Gln	Asp	Phe	Val	Lys	Lys	Glu	Ile	Leu	Asp	Leu	Met	Thr	245	250	255	
Cys	Glu	Pro	Pro	Gln	His	Ala	Thr	Ile	Pro	Leu	Leu	Pro	Asp	Glu	Ile	260	265	270	
Leu	Ala	Lys	Cys	Gln	Ala	Arg	Asn	Ile	Pro	Ser	Leu	Thr	Tyr	Asn	Gln	275	280	285	
Leu	Ala	Val	Ile	Tyr	Lys	Leu	Ile	Trp	Tyr	Gln	Asp	Gly	Tyr	Glu	Gln	290	295	300	
Pro	Ser	Glu	Glu	Asp	Leu	Arg	Arg	Ile	Met	Ser	Gln	Pro	Asp	Glu	Asn	305	310	315	320
Glu	Ser	Gln	Thr	Asp	Val	Ser	Phe	Arg	His	Ile	Thr	Glu	Ile	Thr	Ile	325	330	335	
Leu	Thr	Val	Gln	Leu	Ile	Val	Glu	Phe	Ala	Lys	Gly	Leu	Pro	Ala	Phe	340	345	350	
Thr	Lys	Ile	Pro	Gln	Glu	Asp	Gln	Ile	Thr	Leu	Leu	Lys	Ala	Cys	Ser	355	360	365	

Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser
 370 375 380
 Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr
 385 390 395 400
 Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys
 405 410 415
 Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu
 420 425 430
 Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln
 435 440 445
 Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr
 450 455 460
 Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala
 465 470 475 480
 Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn
 485 490 495
 Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys
 500 505 510
 Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln
 515 520 525
 Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala
 530 535 540
 Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp
 545 550 555 560
 Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln
 565 570 575
 Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp
 580 585 590
 Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln
 595 600 605
 Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln
 610 615 620
 Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala
 625 630 635 640
 Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser
 645 650 655
 Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr
 660 665 670

Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr
675 680 685

Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val
690 695 700

Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu
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Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val
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Ala Val Lys Ser Glu His Ser Thr Thr Ala
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<211> 3126
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GECR

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agt gtg ctt gct cag gag agg gga gat gtg atg gac ttc tat aaa acc 96
Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr
20 25 30

cta aga gga gga gct act gtg aag gtt tct gcg tct tca ccc tca ctg 144
Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
35 40 45

gct gtc gct tct caa tca gac tcc aag cag cga aga ctt ttg gtt gat 192
Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
50 55 60

ttt cca aaa ggc tca gta agc aat gcg cag cag cca gat ctg tcc aaa 240
Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
65 70 75 80

gca gtt tca ctc tca atg gga ctg tat atg gga gag aca gaa aca aaa 288
Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
85 90 95

gtg atg gga aat gac ctg gga ttc cca cag cag ggc caa atc agc ctt 336
Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
100 105 110

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Ser	Ser	Gly	Glu	Thr	Asp	Leu	Lys	Leu	Leu	Glu	Glu	Ser	Ile	Ala	Asn	
		115					120					125				
ctc	aat	agg	tcg	acc	agt	gtt	cca	gag	aac	ccc	aag	agt	tca	gca	tcc	432
Leu	Asn	Arg	Ser	Thr	Ser	Val	Pro	Glu	Asn	Pro	Lys	Ser	Ser	Ala	Ser	
	130					135					140					
act	gct	gtg	tct	gct	gcc	ccc	aca	gag	aag	gag	ttt	cca	aaa	act	cac	480
Thr	Ala	Val	Ser	Ala	Ala	Pro	Thr	Glu	Lys	Glu	Phe	Pro	Lys	Thr	His	
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tct	gat	gta	tct	tca	gaa	cag	caa	cat	ttg	aag	ggc	cag	act	ggc	acc	528
Ser	Asp	Val	Ser	Ser	Glu	Gln	Gln	His	Leu	Lys	Gly	Gln	Thr	Gly	Thr	
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Asn	Gly	Gly	Asn	Val	Lys	Leu	Tyr	Thr	Thr	Asp	Gln	Ser	Thr	Phe	Asp	
			180					185					190			
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Ile	Leu	Gln	Asp	Leu	Glu	Phe	Ser	Ser	Gly	Ser	Pro	Gly	Lys	Glu	Thr	
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Asn	Glu	Ser	Pro	Trp	Arg	Ser	Asp	Leu	Leu	Ile	Asp	Glu	Asn	Cys	Leu	
	210					215					220					
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Leu	Ser	Pro	Leu	Ala	Gly	Glu	Asp	Asp	Ser	Phe	Leu	Leu	Glu	Gly	Asn	
225				230					235					240		
tcg	aat	gag	gac	tgc	aag	cct	ctc	att	tta	ccg	gac	act	aaa	ccc	aaa	768
Ser	Asn	Glu	Asp	Cys	Lys	Pro	Leu	Ile	Leu	Pro	Asp	Thr	Lys	Pro	Lys	
				245				250						255		
att	aag	gat	aat	gga	gat	ctg	gtt	ttg	tca	agc	ccc	agt	aat	gta	aca	816
Ile	Lys	Asp	Asn	Gly	Asp	Leu	Val	Leu	Ser	Ser	Pro	Ser	Asn	Val	Thr	
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ctg	ccc	caa	gtg	aaa	aca	gaa	aaa	gaa	gat	ttc	atc	gaa	ctc	tgc	acc	864
Leu	Pro	Gln	Val	Lys	Thr	Glu	Lys	Glu	Asp	Phe	Ile	Glu	Leu	Cys	Thr	
	275					280						285				
cct	ggg	gta	att	aag	caa	gag	aaa	ctg	ggc	aca	gtt	tac	tgt	cag	gca	912
Pro	Gly	Val	Ile	Lys	Gln	Glu	Lys	Leu	Gly	Thr	Val	Tyr	Cys	Gln	Ala	
	290					295				300						
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Ser	Phe	Pro	Gly	Ala	Asn	Ile	Ile	Gly	Asn	Lys	Met	Ser	Ala	Ile	Ser	
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Val	His	Gly	Val	Ser	Thr	Ser	Gly	Gly	Gln	Met	Tyr	His	Tyr	Asp	Met	
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Asn	Thr	Ala	Ser	Leu	Ser	Gln	Gln	Gln	Asp	Gln	Lys	Pro	Ile	Phe	Asn	
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gtc	att	cca	cca	att	ccc	gtt	ggt	tcc	gaa	aat	tgg	aat	agg	tgc	caa	1104
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gga	tct	gga	gat	gac	aac	ttg	act	tct	ctg	ggg	act	ctg	aac	ttc	cct	1152
Gly	Ser	Gly	Asp	Asp	Asn	Leu	Thr	Ser	Leu	Gly	Thr	Leu	Asn	Phe	Pro	
	370					375				380						
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Gly	Arg	Thr	Val	Phe	Ser	Asn	Gly	Tyr	Ser	Ser	Pro	Ser	Met	Arg	Pro	
385					390					395					400	
gat	gta	agc	tct	cct	cca	tcc	agc	tcc	tca	aca	gca	aca	aca	gga	cca	1248
Asp	Val	Ser	Ser	Pro	Pro	Ser	Ser	Ser	Ser	Thr	Ala	Thr	Thr	Gly	Pro	
				405					410					415		
cct	ccc	agc	ggc	cgc	gtg	caa	gag	gag	ctg	tgc	ctg	gtt	tgc	ggc	gac	1296
Pro	Pro	Ser	Gly	Arg	Val	Gln	Glu	Glu	Leu	Cys	Leu	Val	Cys	Gly	Asp	
			420				425						430			
agg	gcc	tcc	ggc	tac	cac	tac	aac	gcc	ctc	acc	tgt	gga	tcc	tgc	aag	1344
Arg	Ala	Ser	Gly	Tyr	His	Tyr	Asn	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys	
		435					440					445				
gtg	ttc	ttt	cga	cgc	agc	gtt	acg	aag	agc	gcc	gtc	tac	tgc	tgc	aag	1392
Val	Phe	Arg	Arg	Ser	Val	Thr	Lys	Ser	Ala	Val	Tyr	Cys	Cys	Lys		
	450					455				460						
ttc	ggg	cgc	gcc	tgc	gaa	atg	gac	atg	tac	atg	agg	cga	aag	tgt	cag	1440
Phe	Gly	Arg	Ala	Cys	Glu	Met	Asp	Met	Tyr	Met	Arg	Arg	Lys	Cys	Gln	
465					470					475					480	
gag	tgc	cgc	ctg	aaa	aag	tgc	ctg	gcc	gtg	ggt	atg	cgg	ccg	gaa	tgc	1488
Glu	Cys	Arg	Leu	Lys	Lys	Cys	Leu	Ala	Val	Gly	Met	Arg	Pro	Glu	Cys	
			485					490						495		
gtc	gtc	ccg	gag	aac	caa	tgt	gcg	atg	aag	cgg	cgc	gaa	aag	aag	gcc	1536
Val	Val	Pro	Glu	Asn	Gln	Cys	Ala	Met	Lys	Arg	Arg	Glu	Lys	Lys	Ala	
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cag	aag	gag	aag	gac	aaa	atg	acc	act	tcg	ccg	agc	tct	cag	cat	ggc	1584
Gln	Lys	Glu	Lys	Asp	Lys	Met	Thr	Thr	Ser	Pro	Ser	Ser	Gln	His	Gly	
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ggc	aat	ggc	agc	ttg	gcc	tct	ggt	ggc	ggc	caa	gac	ttt	gtt	aag	aag	1632
Gly	Asn	Gly	Ser	Leu	Ala	Ser	Gly	Gly	Gly	Gln	Asp	Phe	Val	Lys	Lys	
	530					535				540						
gag	att	ctt	gac	ctt	atg	aca	tgc	gag	ccg	ccc	cag	cat	gcc	act	att	1680
Glu	Ile	Leu	Asp	Leu	Met	Thr	Cys	Glu	Pro	Pro	Gln	His	Ala	Thr	Ile	
545					550					555					560	

ccg	cta	cta	cct	gat	gaa	ata	ttg	gcc	aag	tgt	caa	gcg	cgc	aat	ata	1728
Pro	Leu	Leu	Pro	Asp	Glu	Ile	Leu	Ala	Lys	Cys	Gln	Ala	Arg	Asn	Ile	
				565					570					575		
cct	tcc	tta	acg	tac	aat	cag	ttg	gcc	gtt	ata	tac	aag	tta	att	tgg	1776
Pro	Ser	Leu	Thr	Tyr	Asn	Gln	Leu	Ala	Val	Ile	Tyr	Lys	Leu	Ile	Trp	
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Tyr	Gln	Asp	Gly	Tyr	Glu	Gln	Pro	Ser	Glu	Glu	Asp	Leu	Arg	Arg	Ile	
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atg	agt	caa	ccc	gat	gag	aac	gag	agc	caa	acg	gac	gtc	agc	ttt	cgg	1872
Met	Ser	Gln	Pro	Asp	Glu	Asn	Glu	Ser	Gln	Thr	Asp	Val	Ser	Phe	Arg	
	610					615					620					
cat	ata	acc	gag	ata	acc	ata	ctc	acg	gtc	cag	ttg	att	gtt	gag	ttt	1920
His	Ile	Thr	Glu	Ile	Thr	Ile	Leu	Thr	Val	Gln	Leu	Ile	Val	Glu	Phe	
625					630				635					640		
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Ala	Lys	Gly	Leu	Pro	Ala	Phe	Thr	Lys	Ile	Pro	Gln	Glu	Asp	Gln	Ile	
				645					650					655		
acg	tta	cta	aag	gcc	tgc	tcg	tcg	gag	gtg	atg	atg	ctg	cgt	atg	gca	2016
Thr	Leu	Leu	Lys	Ala	Cys	Ser	Ser	Glu	Val	Met	Met	Leu	Arg	Met	Ala	
			660					665					670			
cga	cgc	tat	gac	cac	agc	tcg	gac	tca	ata	ttc	ttc	gcg	aat	aat	aga	2064
Arg	Arg	Tyr	Asp	His	Ser	Ser	Asp	Ser	Ile	Phe	Phe	Ala	Asn	Asn	Arg	
			675				680					685				
tca	tat	acg	cgg	gat	tct	tac	aaa	atg	gcc	gga	atg	gct	gat	aac	att	2112
Ser	Tyr	Thr	Arg	Asp	Ser	Tyr	Lys	Met	Ala	Gly	Met	Ala	Asp	Asn	Ile	
	690					695					700					
gaa	gac	ctg	ctg	cat	ttc	tgc	cgc	caa	atg	ttc	tcg	atg	aag	gtg	gac	2160
Glu	Asp	Leu	Leu	His	Phe	Cys	Arg	Gln	Met	Phe	Ser	Met	Lys	Val	Asp	
705					710					715				720		
aac	gtc	gaa	tac	gcg	ctt	ctc	act	gcc	att	gtg	atc	ttc	tcg	gac	cgg	2208
Asn	Val	Glu	Tyr	Ala	Leu	Leu	Thr	Ala	Ile	Val	Ile	Phe	Ser	Asp	Arg	
				725					730					735		
ccg	ggc	ctg	gag	aag	gcc	caa	cta	gtc	gaa	gcg	atc	cag	agc	tac	tac	2256
Pro	Gly	Leu	Glu	Lys	Ala	Gln	Leu	Val	Glu	Ala	Ile	Gln	Ser	Tyr	Tyr	
			740					745					750			
atc	gac	acg	cta	cgc	att	tat	ata	ctc	aac	cgc	cac	tgc	ggc	gac	tca	2304
Ile	Asp	Thr	Leu	Arg	Ile	Tyr	Ile	Leu	Asn	Arg	His	Cys	Gly	Asp	Ser	
		755					760					765				
atg	agc	ctc	gtc	ttc	tac	gca	aag	ctg	ctc	tcg	atc	ctc	acc	gag	ctg	2352
Met	Ser	Leu	Val	Phe	Tyr	Ala	Lys	Leu	Leu	Ser	Ile	Leu	Thr	Glu	Leu	
	770					775					780					

cgt acg ctg ggc aac cag aac gcc gag atg tgt ttc tca cta aag ctc	2400
Arg Thr Leu Gly Asn Gln Asn Ala Glu Met Cys Phe Ser Leu Lys Leu	
785 790 795 800	
aaa aac cgc aaa ctg ccc aag ttc ctc gag gag atc tgg gac gtt cat	2448
Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile Trp Asp Val His	
805 810 815	
gcc atc ccg cca tcg gtc cag tcg cac ctt cag att acc cag gag gag	2496
Ala Ile Pro Pro Ser Val Gln Ser His Leu Gln Ile Thr Gln Glu Glu	
820 825 830	
aac gag cgt ctc gag cgg gct gag cgt atg cgg gca tcg gtt ggg ggc	2544
Asn Glu Arg Leu Glu Arg Ala Glu Arg Met Arg Ala Ser Val Gly Gly	
835 840 845	
gcc att acc gcc ggc att gat tgc gac tct gcc tcc act tcg gcg gcg	2592
Ala Ile Thr Ala Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala	
850 855 860	
gca gcc gcg gcc cag cat cag cct cag cct cag ccc cag ccc caa ccc	2640
Ala Ala Ala Ala Gln His Gln Pro Gln Pro Gln Pro Gln Pro Gln Pro	
865 870 875 880	
tcc tcc ctg acc cag aac gat tcc cag cac cag aca cag ccg cag cta	2688
Ser Ser Leu Thr Gln Asn Asp Ser Gln His Gln Thr Gln Pro Gln Leu	
885 890 895	
caa cct cag cta cca cct cag ctg caa ggt caa ctg caa ccc cag ctc	2736
Gln Pro Gln Leu Pro Pro Gln Leu Gln Gly Gln Leu Gln Pro Gln Leu	
900 905 910	
caa cca cag ctt cag acg caa ctc cag cca cag att caa cca cag cca	2784
Gln Pro Gln Leu Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro	
915 920 925	
cag ctc ctt ccc gtc tcc gct ccc gtg ccc gcc tcc gta acc gca cct	2832
Gln Leu Leu Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro	
930 935 940	
ggt tcc ttg tcc gcg gtc agt acg agc agc gaa tac atg ggc gga agt	2880
Gly Ser Leu Ser Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser	
945 950 955 960	
gcg gcc ata gga ccc atc acg ccg gca acc acc agc agt atc acg gct	2928
Ala Ala Ile Gly Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala	
965 970 975	
gcc gtt acc gct agc tcc acc aca tca gcg gta ccg atg ggc aac gga	2976
Ala Val Thr Ala Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly	
980 985 990	
gtt gga gtc ggt gtt ggg gtg ggc ggc aac gtc agc atg tat gcg aac	3024
Val Gly Val Gly Val Gly Val Gly Gly Asn Val Ser Met Tyr Ala Asn	
995 1000 1005	

gcc cag acg gcg atg gcc ttg atg ggt gta gcc ctg cat tcg cac caa 3072
 Ala Gln Thr Ala Met Ala Leu Met Gly Val Ala Leu His Ser His Gln
 1010 1015 1020

gag cag ctt atc ggg gga gtg gcg gtt aag tcg gag cac tcg acg act 3120
 Glu Gln Leu Ile Gly Gly Val Ala Val Lys Ser Glu His Ser Thr Thr
 1025 1030 1035 1040

gca tag 3126
 Ala

<210> 9
 <211> 1041
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Recombinant
 GEcR

<400> 9
 Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser
 1 5 10 15

Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr
 20 25 30

Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
 35 40 45

Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
 50 55 60

Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
 65 70 75 80

Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
 85 90 95

Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
 100 105 110

Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn
 115 120 125

Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser
 130 135 140

Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His
 145 150 155 160

Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr
 165 170 175

Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp
 180 185 190

Ile	Leu	Gln	Asp	Leu	Glu	Phe	Ser	Ser	Gly	Ser	Pro	Gly	Lys	Glu	Thr	195	200	205
Asn	Glu	Ser	Pro	Trp	Arg	Ser	Asp	Leu	Leu	Ile	Asp	Glu	Asn	Cys	Leu	210	215	220
Leu	Ser	Pro	Leu	Ala	Gly	Glu	Asp	Asp	Ser	Phe	Leu	Leu	Glu	Gly	Asn	225	230	235
Ser	Asn	Glu	Asp	Cys	Lys	Pro	Leu	Ile	Leu	Pro	Asp	Thr	Lys	Pro	Lys	245	250	255
Ile	Lys	Asp	Asn	Gly	Asp	Leu	Val	Leu	Ser	Ser	Pro	Ser	Asn	Val	Thr	260	265	270
Leu	Pro	Gln	Val	Lys	Thr	Glu	Lys	Glu	Asp	Phe	Ile	Glu	Leu	Cys	Thr	275	280	285
Pro	Gly	Val	Ile	Lys	Gln	Glu	Lys	Leu	Gly	Thr	Val	Tyr	Cys	Gln	Ala	290	295	300
Ser	Phe	Pro	Gly	Ala	Asn	Ile	Ile	Gly	Asn	Lys	Met	Ser	Ala	Ile	Ser	305	310	315
Val	His	Gly	Val	Ser	Thr	Ser	Gly	Gly	Gln	Met	Tyr	His	Tyr	Asp	Met	325	330	335
Asn	Thr	Ala	Ser	Leu	Ser	Gln	Gln	Gln	Asp	Gln	Lys	Pro	Ile	Phe	Asn	340	345	350
Val	Ile	Pro	Pro	Ile	Pro	Val	Gly	Ser	Glu	Asn	Trp	Asn	Arg	Cys	Gln	355	360	365
Gly	Ser	Gly	Asp	Asp	Asn	Leu	Thr	Ser	Leu	Gly	Thr	Leu	Asn	Phe	Pro	370	375	380
Gly	Arg	Thr	Val	Phe	Ser	Asn	Gly	Tyr	Ser	Ser	Pro	Ser	Met	Arg	Pro	385	390	395
Asp	Val	Ser	Ser	Pro	Pro	Ser	Ser	Ser	Ser	Thr	Ala	Thr	Thr	Gly	Pro	405	410	415
Pro	Pro	Ser	Gly	Arg	Val	Gln	Glu	Glu	Leu	Cys	Leu	Val	Cys	Gly	Asp	420	425	430
Arg	Ala	Ser	Gly	Tyr	His	Tyr	Asn	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys	435	440	445
Val	Phe	Phe	Arg	Arg	Ser	Val	Thr	Lys	Ser	Ala	Val	Tyr	Cys	Cys	Lys	450	455	460
Phe	Gly	Arg	Ala	Cys	Glu	Met	Asp	Met	Tyr	Met	Arg	Arg	Lys	Cys	Gln	465	470	475
Glu	Cys	Arg	Leu	Lys	Lys	Cys	Leu	Ala	Val	Gly	Met	Arg	Pro	Glu	Cys	485	490	495

Val	Val	Pro	Glu	Asn	Gln	Cys	Ala	Met	Lys	Arg	Arg	Glu	Lys	Lys	Ala	500	505	510
Gln	Lys	Glu	Lys	Asp	Lys	Met	Thr	Thr	Ser	Pro	Ser	Ser	Gln	His	Gly	515	520	525
Gly	Asn	Gly	Ser	Leu	Ala	Ser	Gly	Gly	Gly	Gln	Asp	Phe	Val	Lys	Lys	530	535	540
Glu	Ile	Leu	Asp	Leu	Met	Thr	Cys	Glu	Pro	Pro	Gln	His	Ala	Thr	Ile	545	550	555
Pro	Leu	Leu	Pro	Asp	Glu	Ile	Leu	Ala	Lys	Cys	Gln	Ala	Arg	Asn	Ile	565	570	575
Pro	Ser	Leu	Thr	Tyr	Asn	Gln	Leu	Ala	Val	Ile	Tyr	Lys	Leu	Ile	Trp	580	585	590
Tyr	Gln	Asp	Gly	Tyr	Glu	Gln	Pro	Ser	Glu	Glu	Asp	Leu	Arg	Arg	Ile	595	600	605
Met	Ser	Gln	Pro	Asp	Glu	Asn	Glu	Ser	Gln	Thr	Asp	Val	Ser	Phe	Arg	610	615	620
His	Ile	Thr	Glu	Ile	Thr	Ile	Leu	Thr	Val	Gln	Leu	Ile	Val	Glu	Phe	625	630	635
Ala	Lys	Gly	Leu	Pro	Ala	Phe	Thr	Lys	Ile	Pro	Gln	Glu	Asp	Gln	Ile	645	650	655
Thr	Leu	Leu	Lys	Ala	Cys	Ser	Ser	Glu	Val	Met	Met	Leu	Arg	Met	Ala	660	665	670
Arg	Arg	Tyr	Asp	His	Ser	Ser	Asp	Ser	Ile	Phe	Phe	Ala	Asn	Asn	Arg	675	680	685
Ser	Tyr	Thr	Arg	Asp	Ser	Tyr	Lys	Met	Ala	Gly	Met	Ala	Asp	Asn	Ile	690	695	700
Glu	Asp	Leu	Leu	His	Phe	Cys	Arg	Gln	Met	Phe	Ser	Met	Lys	Val	Asp	705	710	715
Asn	Val	Glu	Tyr	Ala	Leu	Leu	Thr	Ala	Ile	Val	Ile	Phe	Ser	Asp	Arg	725	730	735
Pro	Gly	Leu	Glu	Lys	Ala	Gln	Leu	Val	Glu	Ala	Ile	Gln	Ser	Tyr	Tyr	740	745	750
Ile	Asp	Thr	Leu	Arg	Ile	Tyr	Ile	Leu	Asn	Arg	His	Cys	Gly	Asp	Ser	755	760	765
Met	Ser	Leu	Val	Phe	Tyr	Ala	Lys	Leu	Leu	Ser	Ile	Leu	Thr	Glu	Leu	770	775	780
Arg	Thr	Leu	Gly	Asn	Gln	Asn	Ala	Glu	Met	Cys	Phe	Ser	Leu	Lys	Leu	785	790	795

Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile Trp Asp Val His
 805 810 815

Ala Ile Pro Pro Ser Val Gln Ser His Leu Gln Ile Thr Gln Glu Glu
 820 825 830

Asn Glu Arg Leu Glu Arg Ala Glu Arg Met Arg Ala Ser Val Gly Gly
 835 840 845

Ala Ile Thr Ala Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala
 850 855 860

Ala Ala Ala Ala Gln His Gln Pro Gln Pro Gln Pro Gln Pro Gln Pro
 865 870 875 880

Ser Ser Leu Thr Gln Asn Asp Ser Gln His Gln Thr Gln Pro Gln Leu
 885 890 895

Gln Pro Gln Leu Pro Pro Gln Leu Gln Gly Gln Leu Gln Pro Gln Leu
 900 905 910

Gln Pro Gln Leu Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro
 915 920 925

Gln Leu Leu Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro
 930 935 940

Gly Ser Leu Ser Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser
 945 950 955 960

Ala Ala Ile Gly Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala
 965 970 975

Ala Val Thr Ala Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly
 980 985 990

Val Gly Val Gly Val Gly Val Gly Gly Asn Val Ser Met Tyr Ala Asn
 995 1000 1005

Ala Gln Thr Ala Met Ala Leu Met Gly Val Ala Leu His Ser His Gln
 1010 1015 1020

Glu Gln Leu Ile Gly Gly Val Ala Val Lys Ser Glu His Ser Thr Thr
 1025 1030 1035 1040

Ala

<210> 10

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Modified
 ecdysone response element

<220>
 <221> modified_base
 <222> (4)..(5)
 <223> a, c, t, g, other or unknown

<220>
 <221> modified_base
 <222> (7)..(11)
 <223> a, c, t, g, other or unknown, wherein the length of this
 region may vary in length from 0 to 5, with 1 being
 especially preferred

<220>
 <221> modified_base
 <222> (14)..(15)
 <223> a, c, t, g, other or unknown

<400> 10
 rgbnnmnnnn ntgnncy

17

<210> 11
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Modified
 ecdysone response element

<220>
 <221> modified_base
 <222> (3)..(4)
 <223> a, c, t, g, other or unknown

<220>
 <221> modified_base
 <222> (7)..(11)
 <223> a, c, t, g, other or unknown, wherein the length of this
 region may vary in length from 0 to 5, with 1 being
 especially preferred

<220>
 <221> modified_base
 <222> (13)..(14)
 <223> a, c, t, g, other or unknown

<400> 11
 rgnnccannnn nknnvcy

17

<210> 12
 <211> 13
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Modified
 ecdysone response element

<220>
 <221> modified_base
 <222> (7)
 <223> a, c, t, g, other or unknown

<400> 12
 agtgcantgt tct

13

<210> 13
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Modified
 ecdysone response element

<220>
 <221> modified_base
 <222> (4)..(5)
 <223> a, c, t, g, other or unknown

<220>
 <221> modified_base
 <222> (7)..(11)
 <223> a, c, t, g, other or unknown, wherein the length of this
 region may vary in length from 0 to 5, with 3 being
 especially preferred

<220>
 <221> modified_base
 <222> (15)..(16)
 <223> a, c, t, g, other or unknown

<400> 13
 rgbnnmnnnn nrgbnnm

17

<210> 14
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 14
 tacaacgcc tcacctgtgg atcctgcaag gtgtttcttt cgacgcagc

49

<210> 15
 <211> 53

<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 15

gtactcccg ggcggggcta tgcggggcgg ggctaatacg taggggcggg gca 53

<210> 16

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 16

gtactgccc gccctagcg attagccccg cccgcatag cccgccccg gga 53

<210> 17

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 17

agctcgatg acaagtgc tgttctttgc tgaa 34

<210> 18

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 18

agctttcagc aagagaacaa tgcacttgct catcg 35